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Composition and Functional Diversity of Zooplankton-associated Prokaryote Communities in a Greenlandic Fjord

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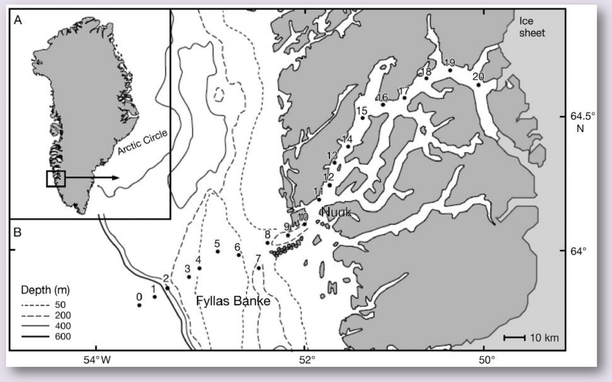
Background

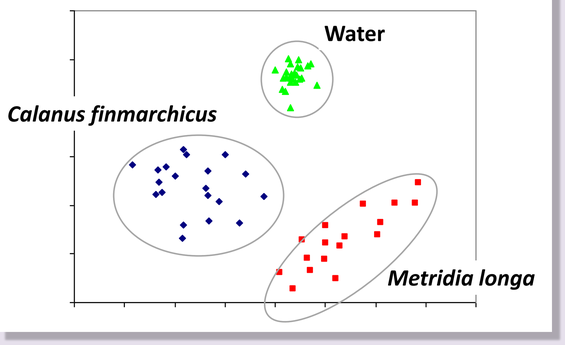
- Prokaryotes densely colonize zooplankton bodies (Tang 2005, Grossart et al. 2009), but they are often poorly sampled or characterized (Tang et al. 2010).
- Greenlandic fjords are very productive ecosystems, but information on free-living and zooplankton-associated prokaryotes there is very limited.
- We compared the prokaryote communities in pelagic water samples and those associated with zooplankton along a salinity gradient in Godthåbsfjord, Greenland (Tang et al. 2011a).



Methods

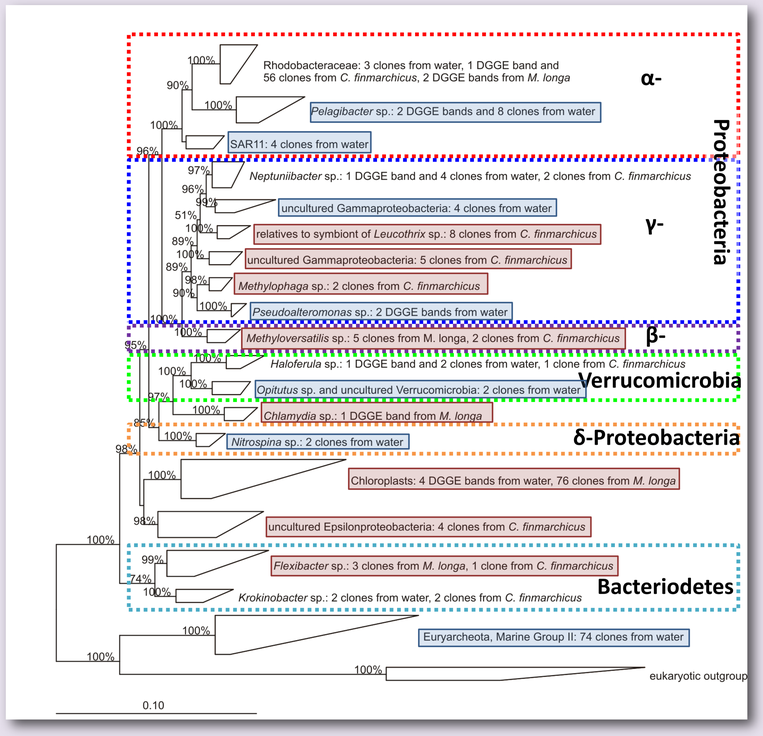
- Surface water and zooplankton samples were collected during the ECOGREEN (2008) and BOFYGO (2010) expeditions in the spring on board R/V Dana.
- Prokaryote community compositions were analyzed by DGGE and clone libraries.
- PCR screening was done to look for specific functional groups.

Multi-dimensional scaling analysis of prokaryote community compositions



- *Calanus*, *Metridia* (calanoid copepods) and water samples formed distinct clusters in terms of prokaryote compositions.
- *Calanus* feeds mainly on diatoms in the spring; *Metridia* feeds omnivorously throughout the year.
- Dietary differences could lead to delivery of different prokaryotes to the two copepod species (Tang 2005, Tang et al. 2009).

Phylogenetic tree of prokaryotes in zooplankton and water samples



PCR screening for specific prokaryote functional groups

Prokaryote group	Functional gene	*Calanus hyperboreus*	*Pareuchaeta sp.*	*Metridia longa*	Chaetognath	Water
Methanogens	*mcrA*	✓		(✓)	✓	
Sulfate reducers	*dsr*	✓			✓	
Nitrogen fixers	*nifH*	✓			✓	
Dentrifiers	*nirK*				✓	
Denitrifiers	*nirS*				✓	
NH_3-oxidizing archaea	*amoA*	✓				✓
Planctomycetes		✓	✓		✓	
Archaea		✓	✓			✓

- Some prokaryote groups were found exclusively in zooplankton.
- Functional genes indicated occurrence of anaerobic microbial processes in zooplankton: methanogenesis, sulfate reduction, nitrogen fixation and denitrification.

Statistical analysis of environmental factors structuring prokaryotic community composition in the water column

	all	salinity	temperature	fluorescence	density	depth	station
Bacteria	R=0.246 p<0.001	R=0.12 p=0.014	R=0.011 p=0.388	R=0.134 p=0.008	R=0.113 p=0.018	R=0.116 p=0.011	R=0.52 p<0.001
Archaea	R=0.137 p=0.018	R=0.143 p=0.020	R=0.051 p=0.203	R=-0.01 p=0.528	R=0.13 p=0.022	R=0.115 p=0.006	R=0.116 p=0.025
α-Proteobacteria	R=0.211 p<0.001	R=0.282 p<0.001	R=0.113 p=0.029	R=0.087 p=0.056	R=0.276 p<0.001	R=0.175 p<0.001	R=0.427 p<0.001
Actinobacteria	R=0.073 p=0.088	R=0.047 p=0.173	R=0.028 p=0.284	R=-0.018 p=0.616	R=0.042 p=0.185	R=0.043 p=0.139	R=0.262 p<0.001

- Mantel-Test revealed spatial variation of community structure of Bacteria, α-Proteobacteria, and Archaea along the salinity gradient.
- Density, depth and station also influenced prokaryotic community structure.

Summary

- Zooplankton-associated prokaryotes increased the overall prokaryote diversity in the water column, consistent with studies in other aquatic systems (Grossart et al. 2009, Tang et al. 2009).
- Anoxic zooplankton guts may support anaerobic microbial activities within the oxygenated water column (Tang et al. 2011b), which was supported by our PCR functional gene analysis.
- Potential changes in plankton compositions in Greenland fjords in response to rapid climate change could lead to corresponding changes in prokaryote diversity and biogeochemical functions.

Outreach Efforts

- Plankton and bacteria are not familiar to Greenlanders, but they are important for sustaining Greenland fisheries.
- We worked with reporters to disseminate our research via internet blogs and local newspaper articles.


June 9
Searching for the invisible habitants of the sea

By Kam W. Tang, Torkel Gissel Nielsen and Birgit Søborg

During the Greenland expedition we will be collecting water and zooplankton samples frequently along a transect from Fyllas Bank to the innermost part of the Godthåbsfjord. We are looking for the invisible and yet obviously important bacteria in the sea.

We will measure bacterial abundances in the samples using a flow cytometer, and bacterial community composition using DNA-based molecular techniques. In addition, we will measure bacterial production using radioisotope.

The study will produce the first high-resolution description of the bacteria in Godthåbsfjord, and ultimately a better understanding of how future climate change may affect the local ecosystem and fisheries production.

Dr. Kam Tang and technician Birgit Søborg are preparing the investigations of the bacterio plankton in the Godthåbs fjord. Photo Torkel Gissel Nielsen.

On-line blog:
http://www.aqua.dtu.dk/English/About/Research_vessel/Greenland_Cruise_2010.aspx

Greenland newspaper article about our research. (Sorry, I can't translate it for you.)


Vandlopper og methanregnskabet
KLIMAARTIKLERNE I KODEN OG DELTAGERNE I BØRSEN
13. nov.
Brussel

- Microbes are not "charismatic megafauna" that K-12 students normally encounter in their curricula.
- Tang worked with his graduate student Samantha Bickel through the NSF-funded **GK-12 PERFECT** project at VIMS to bring microbial ecology into grade 10 classrooms.

GK-12 Fellow in action
Graduate student Samantha Bickel teaches high school students about her research on marine microbes.

For more information, please visit:
http://www.vims.edu/education/teaching/gk12/

Related Oral Presentation

Zooplankton-associated bacterial abundance and community composition in the York River tributary of Chesapeake Bay
Samantha L. Bickel, Kam W. Tang, Hans-Peter Grossart [Abstract 11633; Tuesday 9:15 am, session 153 Ballroom D]

References and Acknowledgements

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